



SEQUENCE LISTING

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TECH CENTER 1600/2900

<110> Herath, et al

<120> Nucleic Acid Molecules, Polypeptides and Uses Therefor, Including  
Diagnosis and Treatment of Alzheimer's Disease

<130> 9195-078

<140> 10/014,340

<141> 2001-12-10

<160> 823

<170> PatentIn version 3.0

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Asp Pro Arg Asn Ile Leu Leu Thr Asn Glu Gln Leu Glu Ser Ala Arg  
35 40 45  
Lys Ile Val His Asp Tyr Arg Gln Gly Ile Val Pro Pro Gly Leu Thr  
50 55 60  
Glu Asn Glu Leu Trp Arg Ala Lys Tyr Ile Tyr Asp Ser Ala Phe His  
65 70 75 80  
Pro Asp Thr Gly Glu Lys Met Ile Leu Ile Gly Arg Met Ser Ala Gln  
85 90 95  
Val Pro Met Asn Met Thr Ile Thr Gly Cys Met Met Thr Phe Tyr Arg  
100 105 110  
Thr Thr Pro Ala Val Leu Phe Trp Gln Trp Ile Asn Gln Ser Phe Asn  
115 120 125  
Ala Val Val Asn Tyr Thr Asn Arg Ser Gly Asp Ala Pro Leu Thr Val  
130 135 140  
Asn Glu Leu Gly Thr Ala Tyr Val Ser Ala Thr Thr Gly Ala Val Ala  
145 150 155 160  
Thr Ala Leu Gly Leu Asn Ala Leu Thr Lys His Val Ser Pro Leu Ile  
165 170 175  
Gly Arg Phe Val Pro Phe Ala Ala Val Ala Ala Ala Asn Cys Ile Asn  
180 185 190  
Ile Pro Leu Met Arg Gln Arg Glu Leu Lys Val Gly Ile Pro Val Thr  
195 200 205  
Asp Glu Asn Gly Asn Arg Leu Gly Glu Ser Ala Asn Ala Ala Lys Gln  
210 215 220  
Ala Ile Thr Gln Val Val Val Ser Arg Ile Leu Met Ala Ala Pro Gly  
225 230 235 240  
Met Ala Ile Pro Pro Phe Ile Met Asn Thr Leu Glu Lys Lys Ala Phe  
245 250 255  
Leu Lys Arg Phe Pro Trp Met Ser Ala Pro Ile Gln Val Gly Leu Val  
260 265 270  
Gly Phe Cys Leu Val Phe Ala Thr Pro Leu Cys Cys Ala Leu Phe Pro  
275 280 285  
Gln Lys Ser Ser Met Ser Val Thr Ser Leu Glu Ala Glu Leu Gln Ala  
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Lys Ile Gln Glu Ser His Pro Glu Leu Arg Arg Val Tyr Phe Asn Lys  
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Gly Leu

<210> 822

<211> 984

<212> DNA

<213> Homo sapiens

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<221> modified\_base

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<223> n = a, c, g, or t

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<223> n = a, c, g, or t

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 tctgttaacc aacgaacaac tcgagagtgc gagaaaaata gtacatgatt acaggcaagg 180  
 aattgttctt cctgggtctta cagaaaatga attgtggaga gcaaagtaca tctatgattc 240  
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 gctgttcttg cagtggatta accagtcctt caatgcccgc gtcaattaca ccaacagaag 420  
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 acgttttgtt ccttttctg cccgtagctgc tgctaattgc attaatattc cattaatgag 600  
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<210> 823

<211> 261

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Met Ser Gly Glu Leu Pro Pro Asn Ile Asn Ile Lys Glu Pro Arg Trp  
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 Asp Gln Ser Thr Phe Ile Gly Arg Ala Asn His Phe Phe Thr Val Thr  
 20 25 30  
 Asp Pro Arg Asn Ile Leu Leu Thr Asn Glu Gln Leu Glu Ser Ala Arg  
 35 40 45  
 Lys Ile Val His Asp Tyr Arg Gln Gly Ile Val Pro Pro Gly Leu Thr  
 50 55 60  
 Glu Asn Glu Leu Trp Arg Ala Lys Tyr Ile Tyr Asp Ser Ala Phe His  
 65 70 75 80  
 Pro Asp Thr Gly Glu Lys Met Ile Leu Ile Gly Arg Met Ser Ala Gln  
 85 90 95  
 Val Pro Met Asn Met Thr Ile Thr Gly Cys Met Met Thr Phe Tyr Arg  
 100 105 110  
 Thr Thr Pro Ala Val Leu Phe Trp Gln Trp Ile Asn Gln Ser Phe Asn  
 115 120 125  
 Ala Val Val Asn Tyr Thr Asn Arg Ser Gly Asp Ala Pro Leu Thr Val  
 130 135 140  
 Asn Glu Leu Gly Thr Ala Tyr Val Ser Val Thr Thr Gly Ala Val Ala  
 145 150 155 160  
 Thr Ala Leu Gly Leu Asn Ala Leu Thr Lys His Val Ser Pro Leu Ile  
 165 170 175  
 Gly Arg Phe Val Pro Phe Ala Ala Val Ala Ala Asn Cys Ile Asn  
 180 185 190  
 Ile Pro Leu Met Arg Gln Ser His Pro Ser Ile His Tyr Glu His Phe  
 195 200 205  
 Gly Lys Glu Ser Leu Phe Glu Glu Val Pro Met Asp Glu Cys Thr His  
 210 215 220

Ser Ser Trp Val Ser Trp Leu Leu Phe Gly Val Cys Tyr Thr Pro Val  
225 230 235 240

Leu Cys Pro Val Ser Ser Glu Lys Phe His Val Cys Asp Lys Leu Gly  
245 250 255

Gly Arg Val Ala Ser  
260